

O. Chernyshev



ENTERED

1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/783,669A

DATE: 03/27/2002

TIME: 14:38:14

Input Set : A:\LEX-0135-USA SEQLIST.TXT

Output Set: N:\CRF3\03272002\I783669A.raw

4 <110> APPLICANT: Walke, D. Wade
 5 Wilganowski, Nathaniel L.
 7 <120> TITLE OF INVENTION: Novel Human Membrane Proteins and Polynucleotides Encoding
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10 <130> FILE REFERENCE: LEX-0135-USA
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/783,669A
 C--> 12 <141> CURRENT FILING DATE: 2001-02-14

12 <150> PRIOR APPLICATION NUMBER: US 60/183,581
 13 <151> PRIOR FILING DATE: 2000-02-18
 15 <160> NUMBER OF SEQ ID NOS: 9
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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20 <211> LENGTH: 594

21 <212> TYPE: DNA

22 <213> ORGANISM: homo sapiens

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27 gccctggctg ggctggtagg aaacggggtt gtgctctggc tcctgggctt ccgcatgcgc	180
28 aggaacgcct tctctgtcta cgtcctcagc ctggccgggg ccgacttcct ctccctctgc	240
29 ttccagatta taaattgcct ggtgtacctc agtaacttct tctgttccat ctccatcaat	300
30 ttccttagct tcttcaccac tgtgatgacc tgtgcctacc ttgcaggcct gagcatgctg	360
31 agcacgcgtca gcaccgagcg ctgcctgtcc gtccctgtgg ccatctggta tcgctgcgcg	420
32 cgccccagac acctgtcagc ggtcgtgtgt gtccctgtct gggccctgtc cctactgctg	480
33 agcatcttgg aaggaagcag tggcggctgc agcagaagtt ctgtggcttc ttatttagtg	540
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37 <211> LENGTH: 197

38 <212> TYPE: PRT

39 <213> ORGANISM: homo sapiens

41 <400> SEQUENCE: 2

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44 Gly Asn Asp Gln Ala Leu Leu Leu Cys Gly Lys Glu Thr Leu Ile	
45 20 25 30	
46 Pro Val Phe Leu Ile Leu Phe Ile Ala Leu Val Gly Leu Val Gly Asn	
47 35 40 45	
48 Gly Phe Val Leu Trp Leu Leu Gly Phe Arg Met Arg Arg Asn Ala Phe	
49 50 55 60	
50 Ser Val Tyr Val Leu Ser Leu Ala Gly Ala Asp Phe Leu Phe Leu Cys	
51 65 70 75 80	
52 Phe Gln Ile Ile Asn Cys Leu Val Tyr Leu Ser Asn Phe Phe Cys Ser	
53 85 90 95	
54 Ile Ser Ile Asn Phe Pro Ser Phe Phe Thr Thr Val Met Thr Cys Ala	

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56 Tyr Leu Ala Gly Leu Ser Met Leu Ser Thr Val Ser Thr Glu Arg Cys
57          115          120          125
58 Leu Ser Val Leu Trp Pro Ile Trp Tyr Arg Cys Arg Arg Pro Arg His
59          130          135          140
60 Leu Ser Ala Val Val Cys Val Leu Leu Trp Ala Leu Ser Leu Leu Leu
61 145          150          155          160
62 Ser Ile Leu Glu Gly Ser Ser Gly Gly Cys Ser Arg Ser Ser Val Ala
63          165          170          175
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77 gccctgggtg ggctggtagg aaacgggttt gtgctctggc tcttgggctt ccgcatgcgc      180
78 aggaacgcct tctctgtcta cgtcctcagc ctggccgggg ccgacttctt ctctctctgc      240
79 ttccagatta taaattgcct ggtgtacctc agtaacttct tctgttccat ctccatcaat      300
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81 agcacccgtc gcaccgagcg ctgacctgtc gtcctgtggc ccatctggta tcgctgccgc      420
82 cgccccagac acctgtcagc ggtcgtgtgt gtcctgtctt gggccctgtc cctactgctg      480
83 agcatcttgg aagggaagtt ctgtggcttc ttatttagtg atggtgactc tgggtggtgt      540
84 cagacatttg atttcacac tgcagcgtgg ctgatttttt tattcatggt tctctgtggg      600
85 tccagtctgg cctgtctggt caggatcctc tgtggctcca ggggtctgcc actgaccagg      660
86 ctgtacctga ccatcctgct cacagtgtct gtgttctctc tctgcggcct gcccttggc      720
87 attcagtggg tctaatatt atggatctgg aaggattctg atgtcttatt ttggcatatt      780
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92 <212> TYPE: PRT
93 <213> ORGANISM: homo sapiens
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98 Gly Asn Asp Gln Ala Leu Leu Leu Leu Cys Gly Lys Glu Thr Leu Ile
99          20          25          30
100 Pro Val Phe Leu Ile Leu Phe Ile Ala Leu Val Gly Leu Val Gly Asn
101          35          40          45
102 Gly Phe Val Leu Trp Leu Leu Gly Phe Arg Met Arg Arg Asn Ala Phe
103          50          55          60
104 Ser Val Tyr Val Leu Ser Leu Ala Gly Ala Asp Phe Leu Phe Leu Cys
105 65          70          75          80
106 Phe Gln Ile Ile Asn Cys Leu Val Tyr Leu Ser Asn Phe Phe Cys Ser
107          85          90          95

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108 Ile Ser Ile Asn Phe Pro Ser Phe Phe Thr Thr Val Met Thr Cys Ala
109           100           105           110
110 Tyr Leu Ala Gly Leu Ser Met Leu Ser Thr Val Ser Thr Glu Arg Cys
111           115           120           125
112 Leu Ser Val Leu Trp Pro Ile Trp Tyr Arg Cys Arg Arg Pro Arg His
113           130           135           140
114 Leu Ser Ala Val Val Cys Val Leu Leu Trp Ala Leu Ser Leu Leu Leu
115 145           150           155           160
116 Ser Ile Leu Glu Gly Lys Phe Cys Gly Phe Leu Phe Ser Asp Gly Asp
117           165           170           175
118 Ser Gly Trp Cys Gln Thr Phe Asp Phe Ile Thr Ala Ala Trp Leu Ile
119           180           185           190
120 Phe Leu Phe Met Val Leu Cys Gly Ser Ser Leu Ala Leu Leu Val Arg
121           195           200           205
122 Ile Leu Cys Gly Ser Arg Gly Leu Pro Leu Thr Arg Leu Tyr Leu Thr
123           210           215           220
124 Ile Leu Leu Thr Val Leu Val Phe Leu Leu Cys Gly Leu Pro Phe Gly
125 225           230           235           240
126 Ile Gln Trp Phe Leu Ile Leu Trp Ile Trp Lys Asp Ser Asp Val Leu
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132 <211> LENGTH: 762
133 <212> TYPE: DNA
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138 gcccttcttc tgctttgtgg caaggagacc ctgatcccg tcttctgat ccttttcatt      120
139 gccctggtcg ggctggtagg aaacgggttt gtgctctggc tcttggtctt ccgcatgcgc      180
140 aggaacgcct tctctgtcta cgtcctcagc ctggccgggg ccgacttcct ctctctctgc      240
141 ttccagatta taaattgcct ggtgtacctc agtaacttct tctgttccat ctccatcaat      300
142 ttccctagct tcttcaccac tgtgatgacc tgtgcctacc ttgcaggcct gagcatgctg      360
143 agcaccgtca gcaccgagcg ctgcctgtcc gtctgtggc ccatctggta tcgctgccgc      420
144 cgccccagac acctgtcagc ggtcgtgtgt gtctgtctt gggccctgtc cctactgctg      480
145 agcatcttgg aaggaagcag tggcggtgc agcagccgat cctcaagctg gctctccaga      540
146 gggctctgca ggacattgct gaggtggatc acagtgaagg atgcttccgt cagggcaccc      600
147 cggagatgtc gagaagcagt ctggtgtaga gatggacagc ctctacttcc atcagatata      660
148 tgtggctttg agaggcaact ttgcccctgt ctgtctgatt tgctgaactt tctcagtcct      720
149 gattttaaaa cagttaagag agtccttgtg aggattaagt ga      762
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152 <211> LENGTH: 253
153 <212> TYPE: PRT
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156 <400> SEQUENCE: 6
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158 1           5           10           15
159 Gly Asn Asp Gln Ala Leu Leu Leu Leu Cys Gly Lys Glu Thr Leu Ile
160           20           25           30

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161 Pro Val Phe Leu Ile Leu Phe Ile Ala Leu Val Gly Leu Val Gly Asn
162          35          40          45
163 Gly Phe Val Leu Trp Leu Leu Gly Phe Arg Met Arg Arg Asn Ala Phe
164          50          55          60
165 Ser Val Tyr Val Leu Ser Leu Ala Gly Ala Asp Phe Leu Phe Leu Cys
166 65          70          75          80
167 Phe Gln Ile Ile Asn Cys Leu Val Tyr Leu Ser Asn Phe Phe Cys Ser
168          85          90          95
169 Ile Ser Ile Asn Phe Pro Ser Phe Phe Thr Thr Val Met Thr Cys Ala
170          100          105          110
171 Tyr Leu Ala Gly Leu Ser Met Leu Ser Thr Val Ser Thr Glu Arg Cys
172          115          120          125
173 Leu Ser Val Leu Trp Pro Ile Trp Tyr Arg Cys Arg Arg Pro Arg His
174          130          135          140
175 Leu Ser Ala Val Val Cys Val Leu Leu Trp Ala Leu Ser Leu Leu Leu
176 145          150          155          160
177 Ser Ile Leu Glu Gly Ser Ser Gly Gly Cys Ser Ser Arg Ser Ser Ser
178          165          170          175
179 Trp Leu Ser Arg Gly Leu Cys Arg Thr Leu Leu Arg Trp Ile Thr Val
180          180          185          190
181 Lys Asp Ala Ser Val Arg Ala Pro Arg Arg Cys Arg Glu Ala Val Trp
182          195          200          205
183 Cys Arg Asp Gly Gln Pro Leu Leu Pro Ser Asp Ile Cys Gly Phe Glu
184          210          215          220
185 Arg Gln Leu Cys Pro Cys Leu Ser Asp Leu Leu Asn Phe Leu Ser Pro
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190 <210> SEQ ID NO: 7

191 <211> LENGTH: 609

192 <212> TYPE: DNA

193 <213> ORGANISM: homo sapiens

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198 gccctggtcg ggctggtagg aaacggggtt gtgctctggc tcctgggctt ccgcatgcgc      180
199 aggaacgcct tctctgtcta cgctctcagc ctggccgggg ccgacttcct ctctctctgc      240
200 ttccagatta taaattgcct ggtgtacctc agtaacttct tctgttccat ctccatcaat      300
201 ttccctagct tcttcaccac tgtgatgacc tgtgcctacc ttgcaggcct gagcatgctg      360
202 agcaccgtca gcaccgagcg ctgcctgtcc gtccctgtgg ccatctggta tcgctgccgc      420
203 cgccccagac acctgtcagc ggtcgtgtgt gtccctgtct gggccctgtc cctactgctg      480
204 agcatcttgg aagggccgat cctcaagctg gctctccaga gggctctgca ggacattgct      540
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209 <211> LENGTH: 202
210 <212> TYPE: PRT
211 <213> ORGANISM: homo sapiens
213 <400> SEQUENCE: 8

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214 Met Asp Pro Thr Thr Pro Ala Trp Gly Thr Glu Ser Thr Thr Val Asn
215 1 5 10 15
216 Gly Asn Asp Gln Ala Leu Leu Leu Leu Cys Gly Lys Glu Thr Leu Ile
217 20 25 30
218 Pro Val Phe Leu Ile Leu Phe Ile Ala Leu Val Gly Leu Val Gly Asn
219 35 40 45
220 Gly Phe Val Leu Trp Leu Leu Gly Phe Arg Met Arg Arg Asn Ala Phe
221 50 55 60
222 Ser Val Tyr Val Leu Ser Leu Ala Gly Ala Asp Phe Leu Phe Leu Cys
223 65 70 75 80
224 Phe Gln Ile Ile Asn Cys Leu Val Tyr Leu Ser Asn Phe Phe Cys Ser
225 85 90 95
226 Ile Ser Ile Asn Phe Pro Ser Phe Phe Thr Thr Val Met Thr Cys Ala
227 100 105 110
228 Tyr Leu Ala Gly Leu Ser Met Leu Ser Thr Val Ser Thr Glu Arg Cys
229 115 120 125
230 Leu Ser Val Leu Trp Pro Ile Trp Tyr Arg Cys Arg Arg Pro Arg His
231 130 135 140
232 Leu Ser Ala Val Val Cys Val Leu Leu Trp Ala Leu Ser Leu Leu Leu
233 145 150 155 160
234 Ser Ile Leu Glu Gly Pro Ile Leu Lys Leu Ala Leu Gln Arg Ala Leu
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236 Gln Asp Ile Ala Glu Val Asp His Ser Glu Gly Cys Phe Arg Gln Gly
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244 <213> ORGANISM: homo sapiens
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249 tgagcatctt gataagcttc actcagtcac caggtttcac tccagatcct gcaggcatct 180
250 ccccatcctc agctgtttgc cagtcccagg aaagcacttc tcaactcacc aactccagta 240
251 gaaagaaggg tgtaaggggg caccagtggg ggttttctga gcatggatcc aaccaccccg 300
252 gcctggggaa cagaaagtac aacagtgaat ggaaatgacc aagcccttct tctgctttgt 360
253 ggcaaggaga ccctgatccc ggtcttctct atccttttca ttgcoctggg cgggctggta 420
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VERIFICATION SUMMARY

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